

Sequence Listing

Sequence No. : 1

Sequence length : 1728

Sequence type : nucleic acid

Strandedness : double

Topology : linear

Molecule type : cDNA to mRNA

Features of sequence

Original source

Organism : pig

Sequence

ATG CGG CCA TGG ACT GGT TCG TGG CGT TGG ATT ATG CTC ATT CTT TTT 48

Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe

1 5 10 15

GCC TGG GGG ACC TTG CTA TTT TAC ATA GGT GGT CAC TTG GTA CGA GAT 96

Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp

20 25 30

AAT GAC CAC TCT GAT CAC TCT AGC CGA GAA CTG TCC AAG ATT TTG GCA 144

Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala

35 40 45

AAG CTG GAA CGC TTA AAA CAA CAA AAT GAA GAC TTG AGG AGA ATG GCT 192

Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala

50 55 60

GAA TCT CTC CGA ATA CCA GAA GGC CCC ATT GAT CAG GGG CCA GCT TCA 240

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser

65 70 75 80

GGA AGA GTT CGT GCT TTA GAA GAG CAA TTT ATG AAG GCC AAA GAA CAG 288

Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln

85 90 95

ATT GAA AAT TAT AAG AAA CAA ACT AAA AAT GGT CCA GGG AAG GAT CAT 336

Ile Glu Asn Tyr Lys Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His

100

105

110

GAA ATC CTA AGG AGG AGG ATT GAA AAT GGA GCT AAA GAG CTC TGG TTT 384

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe

115

120

125

TTT CTA CAA AGT GAG TTG AAG AAA TTA AAG AAT TTA GAA GGA AAT GAA 432

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu

130

135

140

CTC CAA AGA CAT GCA GAT GAA TTT CTA TCA GAT TTG GGA CAT CAT GAA 480

Leu Gln Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu

145

150

155

160

AGG TCT ATA ATG ACG GAT CTA TAC TAC CTC AGT CAA ACA GAT GGG GCA 528

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala

165

170

175

GGT GAT TGG CGT GAA AAG GAG GCC AAA GAT CTG ACA GAG CTG GTC CAG 576

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln

180

185

190

CGG AGA ATA ACA TAT CTT CAG AAT CCC AAG GAC TGC AGC AAA GCC AAG 624

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys

195

200

205

AAG CTA GTG TGT AAT ATC AAC AAA GGC TGT GGC TAT GGC TGT CAG CTC 672

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu

210

215

220

CAT CAT GTA GTG TAC TGC TTT ATG ATT GCA TAT GGC ACC CAG CGA ACA 720

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr

225

230

235

240

CTC GCC TTG GAA TCT CAC AAT TGG CGC TAC GCT ACT GGG GGA TGG GAA 768

Leu Ala Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu

245	250	255	
ACT GTG TTT AGA CCT GTA AGT GAG ACG TGC ACA GAC AGA TCT GGC AGC 816			
Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser			
260	265	270	
TCC ACT GGA CAT TGG TCA GGT GAA GTA AAG GAC AAA AAT GTT CAG GTG 864			
Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val			
275	280	285	
GTT GAG CTC CCC ATT GTA GAC AGT GTT CAT CCT CGT CCT CCA TAT TTA 912			
Val Glu Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu			
290	295	300	
CCC CTG GCT GTC CCA GAA GAC CTT GCA GAT CGA CTT GTA CGA GTC CAT 960			
Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His			
305	310	315	320
GGT GAT CCT GCA GTG TGG TGG GTA TCC CAG TTT GTC AAG TAC TTG ATT 1008			
Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile			
325	330	335	
CGC CCA CAA CCC TGG CTG GAA AAG GAA ATA GAA GAG GCC ACC AAG AAG 1056			
Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys			
340	345	350	
CTA GGC TTC AAA CAT CCA GTT ATT GGA GTC CAT GTT AGA CGC ACA GAC 1104			
Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp			
355	360	365	
AAA GTG GGA GCG GAA GCA GCC TTC CAT CCC ATT GAG GAA TAC ACG GTG 1152			
Lys Val Gly Ala Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Thr Val			
370	375	380	
CAC GTT GAA GAA GAC TTT CAG CTT CTT GCT CGC AGA ATG CAA GTG GAT 1200			
His Val Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp			
385	390	395	400
AAA AAA AGG GTG TAT TTG GCC ACA GAT GAC CCT GCT TTG TTA AAA GAG 1248			

Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu

405

410

415

GCA AAA ACA AAG TAC CCC AGT TAT GAA TTT ATT AGT GAT AAC TCT ATC 1296

Ala Lys Thr Lys Tyr Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser Ile

420

425

430

TCT TGG TCA GCT GGA CTA CAT AAT CGA TAT ACA GAA AAT TCA CTT CGG 1344

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg

435

440

445

GGT GTG ATC CTG GAT ATA CAC TTT CTC TCC CAG GCA GAC TTC CTA GTG 1392

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val

450

455

460

TGT ACT TTT TCA TCG CAG GTC TGT AGA GTT GCT TAT GAA ATC ATG CAA 1440

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln

465

470

475

480

GCG CTG CAT CCT GAT GCC TCT GCG AAC TTC CGT TCT TTG GAT GAC ATC 1488

Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile

485

490

495

TAC TAT TTT GGA GGC CCA AAT GCC CAC AAC CAA ATT GCC ATT TAT CCT 1536

Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro

500

505

510

CAC CAA CCT CGA ACT GAA GGA GAA ATC CCC ATG GAA CCT GGA GAT ATT 1584

His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile

515

520

525

ATT GGT GTG GCT GGA AAT CAC TGG GAT GGC TAT CCT AAA GGT GTT AAC 1632

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn

530

535

540

AGA AAA CTG GGA AGG ACG GGC CTA TAT CCC TCC TAC AAA GTT CGA GAG 1680

Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu

545

550

555

560

AAG ATA GAA ACA GTC AAG TAC CCC ACA TAT CCC GAG GCT GAC AAG TAA 1728

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys

565

570

575

Sequence No. : 2

Sequence length : 575

Sequence type : amino acid

Topology : linear

Molecule type : protein

Sequence

Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe

1

5

10

15

Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp

20

25

30

Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala

35

40

45

Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala

50

55

60

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser

65

70

75

80

Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln

85

90

95

Ile Glu Asn Tyr Lys Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His

100

105

110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe

115

120

125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu

130

135

140

Leu Gln Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu

145	150	155	160
Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala			
	165	170	175
Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln			
	180	185	190
Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys			
	195	200	205
Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu			
	210	215	220
His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr			
	225	230	235
Leu Ala Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu			
	245	250	255
Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser			
	260	265	270
Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val			
	275	280	285
Val Glu Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu			
	290	295	300
Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His			
	305	310	315
Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile			
	325	330	335
Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys			
	340	345	350
Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp			
	355	360	365
Lys Val Gly Ala Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Thr Val			
	370	375	380

His Val Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp			
385	390	395	400
Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu			
405	410	415	
Ala Lys Thr Lys Tyr Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser Ile			
420	425	430	
Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg			
435	440	445	
Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val			
450	455	460	
Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln			
465	470	475	480
Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile			
485	490	495	
Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro			
500	505	510	
His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile			
515	520	525	
Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn			
530	535	540	
Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu			
545	550	555	560
Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys			
565	570	575	

Sequence No. : 3

Sequence length : 26

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His Glu Ile Leu Arg Arg

5

10

15

Arg Ile Glu Asn Gly Ala Lys Glu Leu Gln

20

25

Sequence No. : 4

Sequence length : 10

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys

5

10

Sequence No. : 5

Sequence length : 12

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Lys Tyr Leu Ile Arg Pro Gln Pro Trp Leu Glu Lys

5

10

Sequence No. : 6

Sequence length : 14

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys

5

10

Sequence No. : 7

Sequence length : 19

Sequence type : nucleic acid

Strandedness : single

Topology : linear

Molecule type : DNA

Sequence

AARSAR ACNAA RAAYG GNCC

19

Sequence No. : 8

Sequence length : 20

Sequence type : nucleic acid

Strandedness : single

Topology : linear

Molecule type : DNA

Sequence

TCNGG RTANG TNGGR TAYTT

20

Sequence No. : 9

Sequence length : 2100

Sequence type : nucleic acid

Strandedness : double

Topology : linear

Molecule type : cDNA to mRNA

Features of sequence

Original source

Organism : human

Sequence

	AAGCTTC CTACACATAT	17
CACCAGGAGG ATCTCTTTGA AAGATTC	ACT GCAGGACTAC CAGAGAGAAT AATTTGTCTG	77
AAGCATCATG TGTTGAAACA ACAGAAGTCT	ATTCACCTGT GCACTAACTA GAAACAGAGT	137
TACAATGTTT TCAATTCTTT GAGCTCCAGG	ACTCCAGGGA AGTGAGTTGA AAATCTGAAA	197
ATG CGG CCA TGG ACT GGT TCC TGG CGT	TGG ATT ATG CTC ATT CTT TTT	245
Met Arg Pro Trp Thr Gly Ser Trp Arg	Trp Ile Met Leu Ile Leu Phe	
5	10	15
GCC TGG GGG ACC TTG CTG TTT TAT ATA	GGT GGT CAC TTG GTA CGA GAT	293
Ala Trp Gly Thr Leu Leu Phe Tyr Ile	Gly Gly His Leu Val Arg Asp	
20	25	30
AAT GAC CAT CCT GAT CAC TCT AGC CGA	GAA CTG TCC AAG ATT CTG GCA	341
Asn Asp His Pro Asp His Ser Ser Arg	Glu Leu Ser Lys Ile Leu Ala	
35	40	45
AAG CTT GAA CGC TTA AAA CAG CAG AAT	GAA GAC TTG AGG CGA ATG GCC	389
Lys Leu Glu Arg Leu Lys Gln Gln Asn	Glu Asp Leu Arg Arg Met Ala	
50	55	60
GAA TCT CTC CGG ATA CCA GAA GGC CCT	ATT GAT CAG GGG CCA GCT ATA	437
Glu Ser Leu Arg Ile Pro Glu Gly Pro	Ile Asp Gln Gly Pro Ala Ile	
65	70	75
GGA AGA GTA CGC GTT TTA GAA GAG CAG	CTT GTT AAG GCC AAA GAA CAG	485
Gly Arg Val Arg Val Leu Glu Glu Gln	Leu Val Lys Ala Lys Glu Gln	
85	90	95
ATT GAA AAT TAC AAG AAA CAG ACC AGA	AAT GGT CTG GGG AAG GAT CAT	533
Ile Glu Asn Tyr Lys Lys Gln Thr Arg	Asn Gly Leu Gly Lys Asp His	
100	105	110

GAA ATC CTG AGG AGG AGG ATT GAA AAT GGA GCT AAA GAG CTC TGG TTT	581
Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe	
115 120 125	
TTC CTA CAG AGT GAA TTG AAG AAA TTA AAG AAC TTA GAA GGA AAT GAA	629
Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu	
130 135 140	
CTC CAA AGA CAT GCA GAT GAA TTT CTT TTG GAT TTA GGA CAT CAT GAA	677
Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp Leu Gly His His Glu	
145 150 155 160	
AGG TCT ATA ATG ACG GAT CTA TAC TAC CTC AGT CAG ACA GAT GGA GCA	725
Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala	
165 170 175	
GGT GAT TGG CGG GAA AAA GAG GCC AAA GAT CTG ACA GAA CTG GTT CAG	773
Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln	
180 185 190	
CGG AGA ATA ACA TAT CTT CAG AAT CCC AAG GAC TGC AGC AAA GCC AAA	821
Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys	
195 200 205	
AAG CTG GTG TGT AAT ATC AAC AAA GGC TGT GGC TAT GGC TGT CAG CTC	869
Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu	
210 215 220	
CAT CAT GTG GTC TAC TGC TTC ATG ATT GCA TAT GGC ACC CAG CGA ACA	917
His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr	
225 230 235 240	
CTC ATC TTG GAA TCT CAG AAT TGG CGC TAT GCT ACT GGT GGA TGG GAG	965
Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu	
245 250 255	
ACT GTA TTT AGG CCT GTA AGT GAG ACA TGC ACA GAC AGA TCT GGC ATC	1013
Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ile	

260	265	270	
TCC ACT GCA CAC TGG TCA GGT GAA GTG AAG GAC AAA AAT GTT CAA GTG			1061
Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val			
275	280	285	
GTC GAG CTT CCC ATT GTA GAC AGT CTT CAT CCC CGT CCT CCA TAT TTA			1109
Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu			
290	295	300	
CCC TTG GCT GTA CCA GAA GAC CTC GCA GAT CGA CTT GTA CGA GTG CAT			1157
Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His			
305	310	315	320
GGT GAC CCT GCA GTG TGG TGG GTG TCT CAG TTT GTC AAA TAC TTG ATC			1205
Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile			
325	330	335	
CGC CCA CAG CCT TGG CTA GAA AAA GAA ATA GAA GAA GCC ACC AAG AAG			1253
Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys			
340	345	350	
CTT GGC TTC AAA CAT CCA GTT ATT GGA GTC CAT GTC AGA CGC ACA GAC			1301
Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp			
355	360	365	
AAA GTG GGA ACA GAA GCT GCC TTC CAT CCC ATT GAA GAG TAC ATG GTG			1349
Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val			
370	375	380	
CAT GTT GAA GAA CAT TTT CAG CTT CTT GCA CGC AGA ATG CAA GTG GAC			1397
His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp			
385	390	395	400
AAA AAA AGA GTG TAT TTG GCC ACA GAT GAC CCT TCT TTA TTA AAG GAG			1445
Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu			
405	410	415	
GCA AAA ACA AAG TAC CCC AAT TAT GAA TTT ATT AGT GAT AAC TCT ATT			1493

Ala Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile	
420	425
430	
TCC TGG TCA GCT GGA CTG CAC AAT CGA TAC ACA GAA AAT TCA CTT CGT	1541
Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg	
435	440
445	
GGA GTG ATC CTG GAT ATA CAT TTT CTC TCT CAG GCA GAC TTC CTA GTG	1589
Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val	
450	455
460	
TGT ACT TTT TCA TCC CAG GTC TGT CGA GTT GCT TAT GAA ATT ATG CAA	1637
Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln	
465	470
475	480
ACA CTA CAT CCT GAT GCC TCT GCA AAC TTC CAT TCT TTA GAT GAC ATC	1685
Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile	
485	490
495	
TAC TAT TTT GGG GGC CAG AAT GCC CAC AAT CAA ATT GCC ATT TAT GCT	1733
Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Ile Tyr Ala	
500	505
510	
CAC CAA CCC CGA ACT GCA GAT GAA ATT CCC ATG GAA CCT GGA GAT ATC	1781
His Gln Pro Arg Thr Ala Asp Glu Ile Pro Met Glu Pro Gly Asp Ile	
515	520
525	
ATT GGT GTG GCT GGA AAT CAT TGG GAT GGC TAT TCT AAA GGT GTC AAC	1829
Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn	
530	535
540	
AGG AAA TTG GGA AGG ACG GGC CTA TAT CCC TCC TAC AAA GTT CGA GAG	1877
Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu	
545	550
555	560
AAG ATA GAA ACG GTC AAG TAC CCC ACA TAT CCT GAG GCT GAG AAA TAA	1925
Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys ---	
565	570
575	

AGCTCAGATG GAAGAGATAA ACGACCAAAC TCAGTTCGAC CAAACTCAGT TCAAACCATT 1985
 TCAGCCAAAC TGTAGATGAA GAGGGCTCTG ATCTAACAAA ATAAGGTTAT ATGAGTAGAT 2045
 ACTCTCAGCA CCAAGAGCAG CTGGGAACTG ACATAGGCTT CAATTGGTGG AATTC 2100

Sequence No. : 10

Sequence length : 575

Sequence type : amino acid

Topology : linear

Molecule type : protein

Sequence

Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe

1 5 10 15

Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp

20 25 30

Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala

35 40 45

Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala

50 55 60

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile

65 70 75 80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln

85 90 95

Ile Glu Asn Tyr Lys Lys Gln Thr Arg Asn Gly Leu Gly Lys Asp His

100 105 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe

115 120 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu

130 135 140

Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp Leu Gly His His Glu

145	150	155	160
Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala			
165	170	175	
Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln			
180	185	190	
Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys			
195	200	205	
Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu			
210	215	220	
His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr			
225	230	235	240
Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu			
245	250	255	
Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ile			
260	265	270	
Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val			
275	280	285	
Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu			
290	295	300	
Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His			
305	310	315	320
Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile			
325	330	335	
Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys			
340	345	350	
Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp			
355	360	365	
Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val			
370	375	380	

His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp			
385	390	395	400
Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu			
405	410	415	
Ala Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile			
420	425	430	
Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg			
435	440	445	
Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val			
450	455	460	
Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln			
465	470	475	480
Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile			
485	490	495	
Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Ile Tyr Ala			
500	505	510	
His Gln Pro Arg Thr Ala Asp Glu Ile Pro Met Glu Pro Gly Asp Ile			
515	520	525	
Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn			
530	535	540	
Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu			
545	550	555	560
Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys ---			
565	570	575	

Sequence No. : 11

Sequence length : 14

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile Gly

5

10

Sequence No. : 12

Sequence length : 25

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Lys Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr

5

10

15

Asp Lys Val Gly Thr Glu Ala Ala Phe

20

25

Sequence No. : 13

Sequence length : 13

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser

5

10

Sequence No. : 14

Sequence length : 20

Sequence type : nucleic acid

Strandedness : single

Topology : linear

Molecule type : DNA

Sequence

TTYAA RCAYC CHGTB ATYGG 20

Sequence No. : 15

Sequence length : 20

Sequence type : nucleic acid

Strandedness : single

Topology : linear

Molecule type : DNA

Sequence

GWRTT RTCRG WRATR AAYTC 20